

Cellular Automata and Algorithmic Preprocessing to Improve Clustering

Guide

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Introduction

- With Reversible Cellular Automata acting as natural clusters, we explore the possibility of using reversible CA rules and taking a non-conventional approach towards clustering numerical and categorical datasets, by grouping similar data points based on the rule and cycle formation using cellular automata.
- The goal is to propose a suitable encoding for the dataset, provide an efficient algorithm for clustering the data using the available CA rules and package our method for ease of access and use.

Literature Survey

Reversible Cellular Automata (RCA) clustering

- 1. The reversibility of certain Cellular Automata served as our motivation to explore it as a clustering method for big datasets.
- 2. The properties of Reversible Cellular Automata are exploited for grouping the entities with minimum intra-cluster distance while ensuring that a limited number of cycles exist in the configuration space
- 3. Algorithms of past research perform at par with other state-of-the-art algorithms. [1] [2] [3] [4] [5].

Encoding Techniques

- 1. Real-valued data cannot be processed by a CA. Thus, datasets need to be encoded to binary
- 2. Experimented with encoding algorithms previously used to encode datasets.
 - a. Gödel number encoding [6] assigns a specific number to each symbol and operation within the expression, and combines them using a prime factorization algorithm.
 - b. Entropy-based dimensionality reduction reduces the number of features in high-dimensional data by discarding the least informative ones based on their entropy [7] followed by hashing the numbers using Python's inbuilt hash function SipHash [8] helps reduce number of features and in turn length of binary string
 - c. Other custom encoding techniques were experimented with, involving taking the mean and standard deviation of the data points to aggregate into features of less degree.

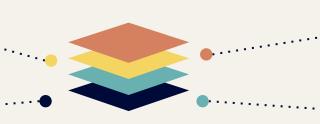
Limitations of Previous Work

- a. Previous algorithms for RCA based clustering exhaustively search for the rules that give best results, leading to extremely long run times.
- b. Previous RCA based clustering algorithms are restricted to a fixed window size, cluster size, and not packaged for ease of usage and access.
- c. Godel number encoding [6] is infeasible as our algorithm's complexity is proportional to the length of the encoded string, and Godel numbers are huge in size
- d. Entropy-based dimensionality reduction [7] followed by hashing the numbers using Python's inbuilt hash function SipHash [8] results in similar data points transforming into vastly different strings.
- e. Other custom encoding techniques were used, resulting in a long string, increasing our complexity.

Objectives/Contributions

Proposed a new encoding algorithm to avoid loss in data and improve the clustering silhouette score.

Proposed a new rule search algorithm that avoids the exhaustive search for rules for a particular dataset.



Packaged the whole process for ease of replication and development.

Provided flexibility and efficiency for multiple datasets with varying number of records and features by saving their states for ease of computation when used again.

Block Diagram

Data Collection

(Different datasets are explored and collected to ensure the algorithm works on all kinds of datasets.)

Data

Pre-Processing

(All raw datasets are converted to numerical data.)

Data Encoding

(The pre-processed dataset is encoded into a binary string using fixed-width BiNCE encoding.)

Analysis of the Results

(The best score out of 10 trials [by default] is displayed. Theories claimed earlier are proven by results.)

Reversible CA Clustering Algorithm

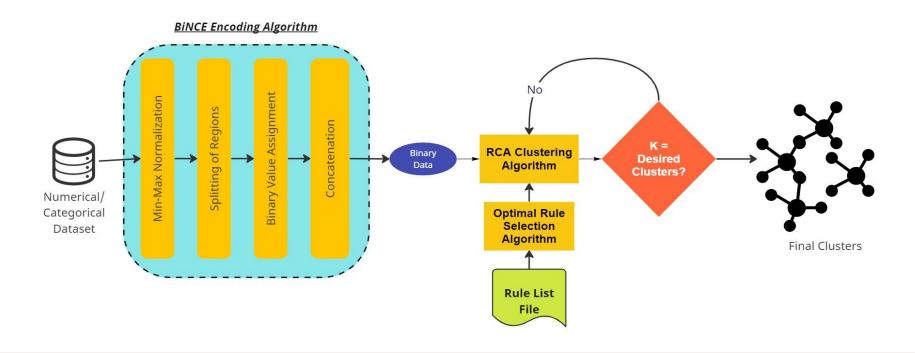
(The encoded binary string is split into chunks and the filtered CA rules are applied till the desired number of clusters are obtained.)

Rule Filtering using Cycle Numbers

(All the cycles for each reversible rule is generated for each split and rules with the smallest number of cycles are selected.)

Data Flow Diagram

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Algorithm of Modules

Encoding Stage

We use our novel **Binary Normalised Ceiling Encoding (BiNCE)** algorithm, a fixed-width encoding technique to encode numerical and categorical datasets into binarized datasets.

Step 1: Normalize the dataset using Min-Max normalization to scale the score between 0 and 1

Step 2: Given the bit size of encoding for each feature, split the 0-1 region into the corresponding parts. For eg. if 2 bit encoding is used, the 0-1 region is then separated into $2^2 = 4$ regions i.e. 0-0.25, 0.25-0.5, 0.5-0.75 and 0.75-1. Similarly, for n-bit encoding, the 0-1 region is split into n regions.

Step 3: Each of these regions is assigned a n-bit binary code in ascending order of value. For eg.

0-0.25 : 00 0.25-0.5 : 01 0.5-0.75 : 10 0.75-1 : 11

Step 4: The features are then concatenated horizontally to get a bitstring representing one single data. Length of the bitstring will be **n*l**, where **n** is the **bit size of each feature** in step 2, and **l** is the **number of features** of each data.

Algorithm of Modules Rule Selection Algorithm

Previous algorithms: Exhaustively apply all rules in search space to get the best score.

Our Rule Selection Algorithm,

Let n be the size of the vertical split, R be the rule set for a window size w, and N_{cyc_a} , N_{cyc_b} be the number of cycles of r_a , $r_b \in R$.

Property: In a given rule set R , there exists $r_a \in R$ with N_{cyc_a} which performs better at clustering for a Reversible Cellular	
Automata, compared to $r_b \in R$ with N_{cyc_b} , where $N_{cyc_a} < N_{cyc}$	- h

This reduces our computation time exponentially as the total number of trials reduces from $^{162}C_2 = 13041$, to $^{20}C_2 = 190$, and in some cases even lower if initial clusters are less than desired clusters.

	Number of
Rule	cycles
3537028050	4
3537035730	8
4031508660	8
3027809415	10
3537972705	10

Number of rules	Combinations	Trials	Time Of Execu tion
162	¹⁶² C ₂	13041	3.6 Hours
20	²⁰ C ₂	190	3.167 mins

^{*} Chosen experimentally to balance the trade-off between speed and accuracy

Algorithm of Modules Clustering Stage

Stage 1: Vertical Splitting:

Here, each encoded binary string of size n is split into equal divisions while padding the last split.

Stage 2: First Level Clustering:

On applying these rules to each of the vertical split, we distribute the partitioned configurations into some preliminary cycles. The (partitioned) configurations under the same cycle form a unique cluster.

Stage 3: Getting Desired Number Of Clusters:

We obtain desired number of clusters by merging the clusters till desired number is reached. We iterate through the clusters to find the smallest cluster and added to other clusters. The best fit for each element is determined by the clusters which give the highest performance index scores [silhouette score]. This procedure is followed till we reach desired number.

Implementation/ Simulation Environment

Environment

- **♦** Python == 3.11.0
- Scikit-learn == 1.2.0
- **♦** Pandas == 1.5.2
- **♦** Numpy == 1.23.5
- Processor: Intel i7 11700K 16M Cache, up to 5.00 GH
- Graphics Card : NVIDIA GeForce RTX A5000 24GB GDDR6
- Disk: 1TB SSD

Datasets

- 1. School District Breakdown Dataset
- 2. Iris Dataset
- 3. Customer Credit Card Information Dataset
- 4. Wine Dataset
- 5. Customer Segmentation Dataset
- 6. Heart Failure

01

Python

For ease of understanding, functional programming, GPU compatibility and replicability of previous papers

02

Numpy and Pandas

For data handling and faster/parallel computations.

03

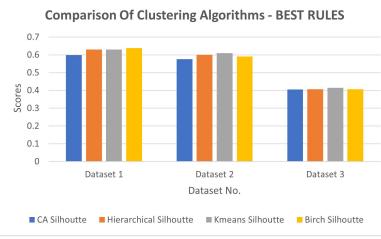
Sklearn

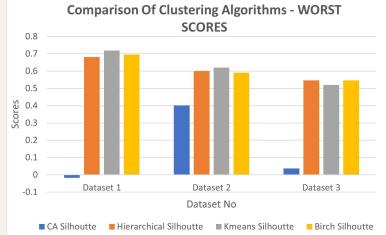
Employing K-Means, Birch and Agglomerative clustering for baseline scores and calculating silhouette scores

Comparison of our CA clustering algorithm using filtered best and worst rules.

Best and Worst 5 results for Dataset 1 with split size 13

Best Rule Set			Worst Rule Set		
Silhouette Score	Rules	Number Of Cycles	Silhouette Score	Worst Rules	Number Of Cycles
	3035673780	44		254611245	3684
0.59742392	3538955760	16	-0.0335495	1259293455	3684
	3035673780	44		256577295	6096
0.5366897	4027576560	64	-0.0534726	1259293455	3684
	3035673780	44		755961615	5156
0.5366897	3785744805	38	-0.0640834	1924428408	5664
	3035673780	44		256577295	6096
0.5217529	4042272240	44	-0.0534726	1259293455	3684
	3035673780	44		254611245	3684
0.5017529	517136850	14	-0.0335495	1259293455	3684

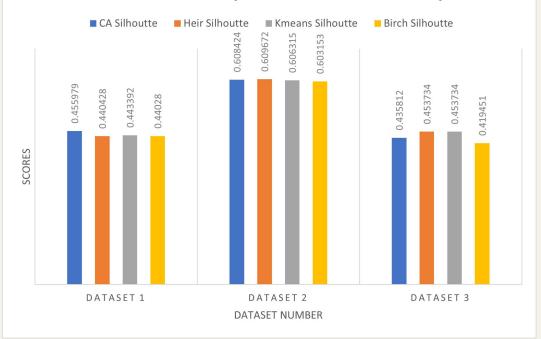




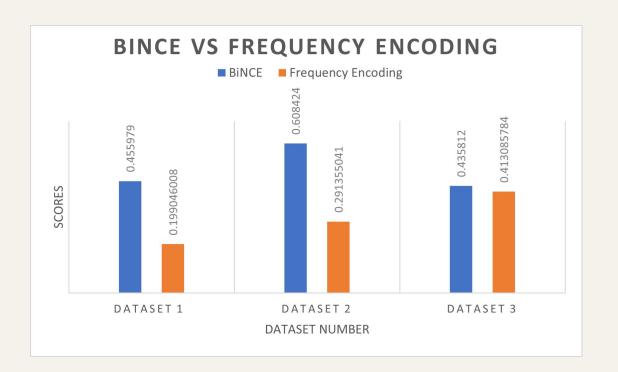
Comparison of our CA clustering algorithm with K-Means, Hierarchical and Birch clustering algorithms to give a better measure of its performance.

Credit Card Customer (Dataset 3)					
RCA	Hier	Kmeans	Birch		
0.435812	0.453734	0.453734	0.419451		
Customer Segmentation					
RCA	Hier	Kmeans	Birch		
0.58454621	0.56822142	0.5834469	0.59377986		
	Heart Failure				
RCA	Hier	Kmeans	Birch		
0.58162802	0.67892885	0.58288851	0.67892885		
Wine Dataset					
RCA	Hier	Kmeans	Birch		
0.46761462	0.6587293	0.65685365	0.6587293		
	IRIS Dataset (Dataset 2)				
RCA	Hier	Kmeans	Birch		
0.60842444	0.60967234	0.6063151	0.60315354		
SDB Dataset (Dataset 1)					
RCA	Hier	Kmeans	Birch		
0.45597978	0.440428	0.443392	0.44028		

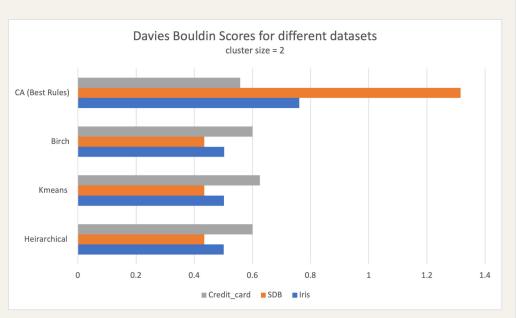
COMPARISON OF CLUSTERING ALGORITHMS (NO. OF CLUSTERS: 2)

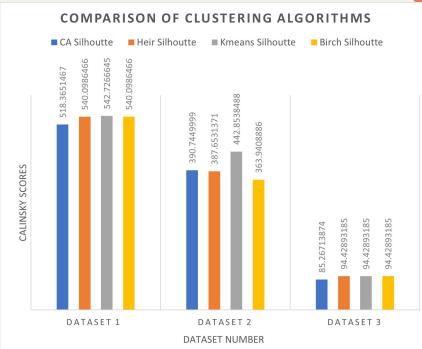


Compared to the previously used **Frequency Based Encoding**, the novel **BiNCE** encoding algorithm results in less loss of data during encoding numerical i.e. floating point and decimal datasets, hence leading to competitive scores with that of state-of-the-art clustering methods.



Comparison of our CA clustering algorithm with K-Means, Hierarchical and Birch clustering algorithms using other clustering metrics





References

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 Reversible Cellular Automata. In Cellular Automata and Discrete Complex Systems: 26th IFIP WG 1.5 International Workshop, AUTOMATA 2020, Stockholm, Sweden, August 10–12, 2020, Proceedings. Springer-Verlag, Berlin, Heidelberg, 29–42.
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- [6] Negadi, Tidjani: "The genetic code via Godel encoding": arXiv preprint arXiv:0805.0695,2008.
- [7] Hong He, Yonghong Tan, "Automatic pattern recognition of ECG signals using entropy-based adaptive dimensionality reduction and clustering", Applied Soft Computing, Volume 55, 2017
- [8] Jean-Philippe Aumasson and Daniel Bernstein. (2012) "SipHash: a fast short- input PRF". In: vol. 7668

Appendix

Packaging of algorithms as Python Modules/ Classes

```
import numpy as np
import pandas as pd
class BiNCE:
   def init (self,dataset,length of each) -> None:
       self.dataset name = 'encoded db'
        self.dataset path = "../../Dataset"
        self.df = dataset
        self.save path = '.temp/Dataset/fixed width encoding '+self.dataset name+'.csv'
        self.length_of_each = length_of_each
        self.even_regions = pow(self.length_of_each, 2)
    def minmaxscale(self.series):
       min val = series.min()
       max val = series.max()
        return (np.divide((np.subtract(series, min_val, dtype=np.float32)), (np.subtract(max_val,min_val, dtype=np.float32))))
    def evenly spaced array(self,num splits)
        return np.linspace(0, 1, num splits+1)[1:]
   def get binary(self, arr2, number):
        idx = np.where(arr2 == number)
        return format(idx[0][0], '0{}b'.format(self.length of each))
   def next greater element(self, x, arr):
       mask = arr >= x
        if any(mask):
           return arr[mask][0]
           return np.nan
   def encode(self):
       for cols in self.df.columns:
           self.df[cols] = self.minmaxscale(self.df[cols])
  self.df[cols] = self.df[cols].fillna(0)
       self.df = self.df.to numpy()
       arr2 = self.evenly_spaced_array(self.even_regions)
       new df = []
       next_greater = []
       for arr1 in self.df:
 ·······next_greater_arr·=·np.array([self.next_greater_element(x, arr2) · for·x·in·arr1])
```

```
import pandas as pd
import numpy as np
from pandas import DataFrame as df
import math, sys, os
import random as rand
from itertools import combinations, permutations
import pickle as pkl
import threading
from sklearn.metrics import silhouette_score,davies_bouldin_score,calinski_harabasz_score
from sklearn.cluster import KMeans, Birch
from sklearn import metrics
import copy
from numpy import random
from sklearn.metrics import silhouette samples, silhouette score
from sklearn.cluster import AgglomerativeClustering
import matplotlib.cm as cm
from multiprocessing import Process
from tabulate import tabulate
import warnings
from bin.BiNCE_encoding import BiNCE
 def __init__(self,Dataset_name,split_size,num_clusters,data_drop_columns, compare_with_others = False, trials = 10,num_threads = 4) -> None:
    self.save_location = '.temp/'
    self.trials = trials
    self.num threads = num threads
    self.Dataset_name = Dataset_name
    self.split_size = split_size
    self.num_clusters = num_clusters
    self.split index = 0
    self.compare = compare with others
    self.data_drop_columns = data_drop_columns
    warnings.filterwarnings("ignore")
```



Appendix

Rule application and Driver functions

```
def apply_rule(self, split,winsize,brule):
 final array = []
 split list=list(set(split))
 split list.sort(reverse=True)
  split_len=len(split_list[0])
 current_array=[]
  while(split list):
   curr element=split list[0]
   flag=0
   while(not flag):
     if current array == []:
       current array, append(curr element)
       split list.remove(curr element)
       curr_element=self.nullbound(split_len,winsize,curr_element)
       for j in range(split_len):
         check=int(str(curr_element[j:j+winsize]),2)
         t2+=brule[check]
       curr element=t2
       if curr_element not in current_array;
           if curr_element in split_list:
             split_list.remove(curr_element)
             current_array.append(curr_element)
           flag=1
   final_array.append(current_array)
   current arrav=[]
 return final array
```

```
def fit(self):
rule_list_name = self.rule_kind+'_cycles_'+str(self.split_size)
os.makedirs('./'+self.save location+self.Dataset_name+'/Custers-'+str(self.num_clusters)+'/Final Clusters', exist_ok=True)
 os.makedirs('./config/'+self.Dataset_name+'/Custers-'+str(self.num_clusters), exist_ok=True)
self.data=pd.read csv("./data/"+self.Dataset name+".csv")
self.data=self.data.dropna()
 self.data=self.data.drop(self.data_drop_columns,axis=1)
window size = 5
encoder = BiNCE(self.data, length of each=2)
 self.enc = encoder.encode()
self.enc = list(self.enc[self.enc.columns[0]])
print(self.enc)
split_enc, num_of_splits = self.split_string(self.enc,self.split_size)
rule_list = self.get_rule_list('./rules/'+rule_list_name+'.txt')
rules_comb = list(combinations(rule_list, 2))
thread pool = []
 rules comb = np.array(rules comb)
rules_comb = rules_comb(:len(rules_comb))
rules sep = np.array split(rules comb,(self.num threads))
 for iclust in range(self.num threads):
  print('Thread : '.iclust)
   init_clusters_ = threading.Thread(target=self.cellular_automata_clustering, args=(num_of_splits, rules_sep[iclust], split_enc, iclust, self.trials, window_size))
   init clusters .daemon = True
   init clusters .start()
   thread_pool.append(init_clusters_)
 for iclust in thread pool:
   iclust.join()
```

Appendix

GitHub Repository

